

SEQUENCE LISTING

<110>	THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES Zoon, Kathryn C. Hu, Renqiu	
	Bekisz, Joseph B.	
	Hayes, Mark P.	
<120>	Interferon Alpha Hybrids	
<130>	4239-64129-01	•
<140>	US 10/615,723	
<141>	2003-07-08	
<150>	US 09/744,754	
<151>	2001-01-24	
<150>	US 60/094,407	
<151>	1998-07-28	
<150>	PCT/US99/15284	
<151>	1999-07-06	
<160>	44	
<170>	PatentIn version 3.1	
<210>		
<211>		
<212><213>	Artificial Sequence	
<220>	Comphania Olicanual carida	
<223>	Synthetic Oligonucleotide	
<400>		0.7
tccgga	tcct gtgatctgcc tcagacc	27
<210>		
<211><212>		
	Artificial Sequence	
(213)	Arciriciar bequence	
<220>	Companya of the Companya of th	
<223>	Synthetic Oligonucleotide	
<400>		27
aycagai	tgag tcctttgtgc tgaagag	27
<210>	3	
<211>	27	
<212>	DNA	

<213> Artificial Sequence

<220> <223>	Synthetic Oligonucleotide	
<400>	3	
	agca caaaggactc atctgct	27
<210>	$oldsymbol{\Lambda}$	
<211>		
<212>		
<213>	Artificial Sequence	
222		
<220>	Synthetic Oligonucleotide	
\ZZ3/	bynchecte original creotiae	
<400>	4	
gagctc	gcat gctcatcatt ccttacttct taaact	36
<210>	5	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
	Synthetic Oligonucleotide	
<400>		
cacgca	ggcc tcgaggtcat tcag	24
	•	
<210>	6	
<211>	24	
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Synthetic Oligonucleotide	
.400.		
<400>	в gacc tcgaggcctg cgtg	24
ocgaac	gace eegaggeeeg egeg	
<210>	7	
<211> <212>		
	Artificial Sequence	
- -		
<220>		
<223>	Synthetic Oligonucleotide	
<400>	7	
	gcat gctcatcatt ccttcctcct taatct	36
<210>	8	

```
<211>
      500
<212>
      DNA
<213> Artificial Sequence
<220>
<223>
      Gene Fusion
<220>
<221>
       CDS
      (1)...(498)
<222>
<400> 8
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata
                                                                        48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
                                                         15
                5
                                     10
1
ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac
                                                                        96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
                                                     30
            20
                                 25
aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc
                                                                      144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
                                                 45
        35
                            40
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc
                                                                       192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
    50
                                             60
                        55
ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc
                                                                       240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
                                         75
                                                             80
                    70
65
ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg
                                                                       288
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
                                     90
                                                         95
                85
gaa gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg
                                                                       336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
                                                     110
            100
                                 105
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act
                                                                       384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
                            120
                                                 125
        115
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc
                                                                       432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
    130
                        135
                                             140
                                                                       480
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
                                                             160
                                         155
145
                    150
                                                                       500
agt tta aga agt aag gaa tg
Ser Leu Arg Ser Lys Glu
```

165

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 9

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 155 160

Ser Leu Arg Ser Lys Glu 165

<210> 10

<211> 500

<212> DNA <213> Artificial Sequence	
<220> <223> Gene Fusion	
<220> <221> CDS <222> (1)(498)	
<pre><400> 10 tgt gat ctg cct cag acc cac agc ctg ggt Cys Asp Leu Pro Gln Thr His Ser Leu Gly 1</pre>	
ctc ctg gca caa atg gga aga atc tct cct Leu Leu Ala Gln Met Gly Arg Ile Ser Pro 20 25	
aga cat gac ttt gga ttc ccc cag gag gag Arg His Asp Phe Gly Phe Pro Gln Glu Glu 35 40	
cag aag gct caa gcc atc tct gtc ctc cat Gln Lys Ala Gln Ala Ile Ser Val Leu His 50 55	
ttc aat ctc ttc agc aca aag gac tca tct Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser 65 70	
ctc cta gaa aaa ttt tcc act gaa ctt aac Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn 85 90	
gag gcc tgt gtg ata càg ggg gtg ggg gtg Glu Ala Cys Val Ile Gln Gly Val Gly Val 100 105	
aag gag gac tcc att ctg gct gtg agg aaa Lys Glu Asp Ser Ile Leu Ala Val Arg Lys 115 120	s Tyr Phe Gln Arg Ile Thr
ctc tat ctg aaa gag aag aaa tac agc cct Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro 130 135	
aga gca gaa atc atg aga tct ttt tct ttg Arg Ala Glu Ile Met Arg Ser Phe Ser Leu 145 150	
agt tta aga agt aag gaa tg Ser Leu Arg Ser Lys Glu 165	500

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 11

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser 65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 150

Ser Leu Arg Ser Lys Glu 165

<210> 12

<211> 497

<212> DNA

<21	3 > <i>i</i>	Arti	ficia	al S	equei	nce								
<22 <22		Gene	Fus	ion										
	1> (CDS (1).	. (49	5)										
tgt	_	ctg								agg Arg				48
										tcc Ser				96
										ggc Gly				144
_	_	_				_			_	atc Ile 60	_	_		192
			_							tgg Trp				240
	_					_				ctg Leu				288
_	_			_		_		 _		act Thr				336
										caa Gln				384
	_			-			-			tgg Trp 140				432
-										att Ile				480
		agg Arg	_	gaa Glu 165	tg									497

<211> 165

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 13

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp 20 25 30

Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln 35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe 50 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn 100 105 110

Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu 115 120 125

Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg 130 135 140

Leu Arg Arg Lys Glu 165

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220> <223>	Synthetic Oligonucleotide	
<400>	14	
gctgct	tggg atgagaccct ccta	24
<210>	15	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
	Synthetic Oligonucleotide	
<400>	15	
taggag	ggtc tcatcccaag cagc	24
<210>	16	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Synthetic Oligonucleotide	
<400>	16	
	aaat tctacactga actctaccag	30
J		
<210>	17	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic Oligonucleotide	
<400>	17	
ctggtag	gagt tcagtgtaga atttgtctag	30
<210>	1 Ω	
<210> <211>		
<211>		
	Artificial Sequence	
<220>		
	Synthetic Oligonucleotide	
<400>	18	
	gacc tcgaggcctg cgtg	24
.		
<210>	19	

<211> <212>		
<213>	Artificial Sequence	
<220> <223>	Synthetic Oligonucleotide	
<400>	ggcc tegaggteat teag	24
<210>		
<211><212>	·	
	Artificial Sequence	
<220>		
<223>	Synthetic Oligonucleotide	
<400>		0.1
gaaaaa	tttt acactgaact t	21
<210>	21	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Synthetic Oligonucleotide	
<400>		
aagttc	agtg taaaattttt c	21
<210>	22	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Synthetic Oligonucleotide	
<400>		21
actgaa	cttt accagcagct g	21
<210>	23	
	21	
<212>	DNA .	
<213>	Artificial Sequence	
<220>		
<223>	Synethetic Oligonucleotide	
	23	ź1
LayCLG	ctgg taaagttcag t	~ _

<210>	24	
<211>	21	
<212>	DNIA	
<213>	Artificial Sequence	
<220>		
	Completia Oliannalectide	
<443>	Synthetic Oligonucleotide	
<400>	24	
gacaaa	ttct ccactgaact c	21
gacaaa	title courtinguities of	
<210>	25	
<211>	21	
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Synthetic Oligonucleotide	
<400>	25	
		21
gagttc	agtg gagaatttgt c	21
<210>	26	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
(213)	THE CITE OF THE CONTROL OF THE CITE OF THE	
<220>		
<223>	Synthetic Oligonucleotide	
400		
<400>		
actgaad	ctca accagcagct g	21
_		
<210>	27	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
	Synthetic Oligonucleotide	
<2237	synchetic origonatieotiae	
<400>	27	
caacta	ctgg ttgagttcag t	21
cageeg	segg regageedag e	
	•	
<210>	28	
<211>		
<212>	DNA	
<213>	Artificial Sequence	
	•	
000		
<220>		
<223>	Synthetic Oligonucleotide	

<400> 28 gagctcgcat gctcatcatt ccttacttct taaact						
<210> 29 <211> 500 <212> DNA <213> Artificial Sequence						
<220> <223> Gene Fusion						
<220> <221> CDS <222> (1)(498)						
<pre><400> 29 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1</pre>	48					
ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30	96					
aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45	144					
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 55 60	192					
ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 65 70 75 80	240					
ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu 85 90 95	288					
gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110	336					
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125	384					
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140	432					
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 155 160	480					

agt tta aga agt aag gaa tg Ser Leu Arg Ser Lys Glu 165

<210> 30

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 30

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35.

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 155 160

Ser Leu Arg Ser Lys Glu

```
<210> 31
<211> 500
<212> DNA
<213> Artificial Sequence
<220>
<223>
      Gene Fusion
<220>
<221> CDS
<222> (1)..(498)
<400> 31
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata
                                                                        48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
                                                         15
                                     10
1
ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac
                                                                        96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
                                25
                                                     30
            20
                                                                       144
aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
                                                 45
        35
                            40
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc
                                                                       192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
                                             60
    50
                        55
                                                                       240
ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
                                                             80
                    70
                                         75
65
                                                                       288
ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctc
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
                                                         95
                85
                                     90
gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg
                                                                       336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
            100
                                                     110
                                105
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act
                                                                       384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
                            120
                                                 125
        115
                                                                       432
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
                                             140
    130
                        135
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa
                                                                       480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
                                         155
                                                             160
                    150
145
```

agt tta aga agt aag gaa tg Ser Leu Arg Ser Lys Glu 165

<210> 32

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 32

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 1 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 155 160

Ser Leu Arg Ser Lys Glu 165

<210> 33 <211> 500 <212> DNA <213> Artificial Sequence	
<220> <223> Gene Fusion	
<220> <221> CDS <222> (1)(498)	
<pre><400> 33 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15</pre>	48
ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30	96
aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45	144
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 55 60	192
ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 65 70 75 80	240
ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu 85 90 95	288
gaa gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met 100 105 110	336
aat gtg gac tcc atc ttg gct gtg aag aaa tac ttc caa aga atc act Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr 115 120 125	384
ctt tat ctg aca gag aag aaa tac agc cct tgt gct tgg gag gtt gtc Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140	432
aga gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu 145 150 155 160	480
aga tta agg agg aag gaa tg	500

Arg Leu Arg Arg Lys Glu 165

<210> 34

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 34

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 65 . 70 . 75 . 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu 85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met 100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu 145 150 150

Arg Leu Arg Arg Lys Glu 165

<210> 35 <211> 500 <212> DNA Artificial Sequence <213> <220> Gene Fusion <223> <220> <221> CDS (1)..(498) <222> <400> 35 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 10 15 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 30 25 20 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 40 45 35 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 55 60 50 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 80 65 75 70 ctc cta gaa aaa ttt tac act gaa ctt aac cag cag ctg aat gac ctc 288 Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu 95 90 85 336 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 110 100 105 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 125 120 115 432 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 140 130 135 480 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 160 145 150 155 500 agt tta aga agt aag gaa tg Ser Leu Arg Ser Lys Glu

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 36

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 / 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu 165

```
<210> 37
<211> 500
<212> DNA
      Artificial Sequence
<213>
<220>
       Gene Fusion
<223>
<220>
<221>
       CDS
<222>
      (1)..(498)
<400> 37
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata
                                                                        48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
                                     10
1
                                                          15
                                                                        96
ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
            20
                                 25
                                                     30
aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc
                                                                       144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
        35
                             40
                                                 45
                                                                       192
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
    50
                         55
                                             60
ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc
                                                                       240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65
                    70
                                         75
                                                              80
ctc cta gaa aaa ttt tcc act gaa ctt tac cag cag ctg aat gac ctc
                                                                       288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
                                     90
                85
                                                                       336
gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
                                                     110
            100
                                 105
                                                                       384
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
        115
                             120
                                                 125
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc
                                                                       432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
    130
                         135
                                             140
                                                                       480
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
                                         155
                                                              160
145
                    150
                                                                       500
agt tta aga agt aag gaa tg
Ser Leu Arg Ser Lys Glu
                165
```

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 38

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr 65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 150

Ser Leu Arg Ser Lys Glu 165

<210> 39

```
500
<211>
<212>
       DNA
<213> Artificial Sequence
<220>
<223>
       Gene Fusion
<220>
<221>
       CDS
      (1)..(498)
<222>
<400> 39
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata
                                                                        48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
                                     10
                                                         15
                5
1
ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac
                                                                        96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
                                                     30
            20
                                 25
aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc
                                                                       144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
                                                 45
        35
                             40
                                                                       192
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
                                             60
    50
                         55
ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc
                                                                       240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
                                         75
                                                              80
                    70
65
ctc cta gac aaa ttc tcc act gaa ctc tac cag cag ctg aat gac ctc
                                                                       288
Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
                                                         95
                                     90
                85
gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg
                                                                       336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
                                                     110
            100
                                 105
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act
                                                                       384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
                            120
                                                 125
        115
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc
                                                                       432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
                        135
                                             140
    130
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa
                                                                       480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
                                         155
                                                              160
                    150
145
                                                                       500
agt tta aga agt aag gaa tg
Ser Leu Arg Ser Lys Glu
                165
```

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 40

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 1 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser 65 70 75 80

Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 155 160

Ser Leu Arg Ser Lys Glu 165

<210> 41 <211> 500

<212> DNA <213> Artifi	icial Sequence			
<220> <223> Gene F	Fusion			
<220> <221> CDS <222> (1)((498)			
• •			aat agg agg gcc Asn Arg Arg Ala	
Leu Leu Ala G			ttc tcc tgc ctg Phe Ser Cys Leu 30	
	Phe Gly Phe Pro		ttt gat ggc aac Phe Asp Gly Asn 45	
	_	_	gag atg atc cag Glu Met Ile Gln 60	_
	_	•	gct act tgg gaa Ala Thr Trp Glu 75	
_		_	cag cag ctg aat Gln Gln Leu Asn	
Glu Ala Cys V		•	aca gag act ccc Thr Glu Thr Pro 110	
Lys Glu Asp S		Val Arg Lys	tac ttc caa aga Tyr Phe Gln Arg 125	_
_		_	tgt gcc tgg gag Cys Ala Trp Glu 140	
		_	tca aca aac ttg Ser Thr Asn Leu 155	_
agt tta aga a Ser Leu Arg S	igt aag gaa tg Ser Lys Glu 165			500

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> Gene Fusion

<400> 42

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu 145 150 155 160

Ser Leu Arg Ser Lys Glu 165

<210> 43

<211> 14

<212> PRT

```
<213> Artificial Sequence
<220>
<223> Synthetic peptide
<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid
<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid
<400> 43
Leu Asp Lys Phe Xaa Thr Glu Leu Xaa Gln Gln Leu Asn Asp
1
                5
                                    10
<210> 44
<211> 14
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic peptide
<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid
<220>
<221> misc_feature
<222>
      (9)..(9)
<223> Xaa can be any naturally occurring amino acid
<400> 44
Leu Glu Lys Phe Xaa Thr Glu Leu Xaa Gln Gln Leu Asn Asp
```

10